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Figure 1

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>sp|P47901|V1BR_HUMAN VASOPRESSIN V1B RECEPTOR (AVPR V1B) (VASOPRESSIN V3
    RECEPTOR) (AVPR V3) (ANTIDIURETIC HORMONE RECEPTOR 1B).
    Length = 424

Score = 316 (111.2 bits), Expect = 3.7e-41, Sum P(2) = 3.7e-41
Identities = 70/194 (36%), Positives = 115/194 (59%)

Query:   56 LWVLFVFTIVGNSVVLFTWRR-KKKSRTFFVTQLAITDSFTGLVNILTDINWRFTGDF 114
          L + V   GN VL + + +K+SRM FV LA+TD   L +L + W T F
Sbjct:   41 LATVLVLATGGNLAVLLTLGQLGRKSRMHFLVHLALTDLAVALFQVLPQLLWDITYRF 100

Query:   115 TAPDLVCRVVRYLQVVLLYASTYVLVLSIDRYHAIVYPMKFLQGEKQARVLIVIA-WSL 173
          PDL+CR V+YLQV+ ++ASTY+L+++++DRY A+ +P++ LQ   Q+  L++ A W L
Sbjct:   101 QGPDLLCRAVKYLQVLSMFASTYMLLAMTLDRYLAVCHPLRSLQQPGQSTYLLIAAPWLL 160

Query:   174 SFLFSIPTLIIFGKRTL--SNGEVQCWALWPDDSY-WTP--YMTIVAFLVYFIPLTIISI 228
          + +FS+P + IF R +   +G + CWA  D + W P Y+T   ++ +P+T+++
Sbjct:   161 AAIFSLPQVFIFSLREVIQSGVLCWA---DFGFPWGPRLYLTWTTLAIFVLPVTMLTA 217

Query:   229 MYGIVIRTIW--IKSKT 243
          Y ++   I   +K KT
Sbjct:   218 CYSLICHEICKNLKVKT 234

Score = 131 (46.1 bits), Expect = 3.7e-41, Sum P(2) = 3.7e-41
Identities = 33/80 (41%), Positives = 47/80 (58%)

Query:   258 SSYNRGLISKAKIKAIKYSIIIIILAFICCWSPYF---LFDILDNFNLLPDTQERFYASVI 314
          SS N   IS+AKI+ +K + +I+LA+I CW+P+F   ++ + D N PD   A I
Sbjct:   267 SSINT--ISRAKIRTVKMTFVIVLAYIACWAPFFSVQMWSVWDK-NA-POEDSTNVAFTI 322

Query:   315 IQNLPALNSAINPLIYCVFSSSI 337
          L LNS NP IY F+S +
Sbjct:   323 SMLLGNLNSCCNPWIYMGFNHSL 345

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Figure 2

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>sp|P31388|5H6_RAT 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)
(ST-B17).
Length = 436

Score = 224 (78.9 bits), Expect = 6.7e-17, P = 6.7e-17
Identities = 84/309 (27%), Positives = 144/309 (46%)

Query:   3 PGEA--LLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLLAALDM 60
          PG + + A L V+++ A ++ L++L C A LR S LV+L L++ + M
Sbjct:  23 PGGSGWVAAALCVVIVLTAAANSLIVLICTQPA-LRN-TSNFFLVSLFTSDLMVGLVVM 80

Query:  61 PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLR- 119
          P +L + GR A G C + D S + L++ +S D++L + PLRY R+
Sbjct:  81 PPAMLNLYGRWVLARGLCLLWTAFDVMCCSASILNCLISLDRYLLILSPLRYKLRMTA 140

Query:  120 PRYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAA---FTATL 176
          PR L+LG AW SLA AL S+L + P P + R A F
Sbjct:  141 PRALALILG-AW--SLA----ALA-SFLPLLLGWHELKARTPAPGQCRLLASLPFVLVA 192

Query:  177 HAVGFVLPLAVLCLTSLQVHRVARRHCQRMDTVT-----MKALALLADLHPSVR---- 225
          V F LP +C T ++ AR+ ++ ++T ++ L + P +
Sbjct:  193 SGVTFFLPSGAICFTYCRILLAARKQAVQVASLTGTAGQALETQVPRTPRPGMESADS 252

Query:  226 QRCLIQKRRRRHRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYS 285
          +R + R+ +A+ +GI + F + + P+ + +A+ V + +L+ L Y
Sbjct:  253 RRLATKHSRKALKASLTGILLGMFFVTWLPFFVANIAQAVCDCISPGLFDVLT-WLGYC 311

Query:  286 KAVADPFTYSLLRRPFRQVL 305
          + +P Y L R F++ L
Sbjct:  312 NSTMNPIIYPLFMRDFKRAL 331

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Figure 3

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>sp|P56479|GALR_MOUSE GALANIN RECEPTOR TYPE 1 (GAL1-R) (GALR1).
      Length = 348

Score = 269 (94.7 bits), Expect = 7.9e-24, P = 7.9e-24
Identities = 82/289 (28%), Positives = 136/289 (47%)

Query:   49 VGFVGNLCVIGILLHNAWKGP-SMIHSLILNLSLADLSLLLFSAPIRATAYSKSVWDLG 107
          +G +GN VI +L + GKP S + ILNLS+ADL+ LLF P +AT Y+ W LG
Sbjct:   46 MGVLGNSLVITVLARSK-PGKPRSTTNLFILNLSIADLAYLLFCIPFQATVYALPTWVLG 104

Query:  108 WfVCKSSDWFIHTCMAAKSLTIVVVA--KVCfMYASDPAKQVSIHNYTIWSVLVAIWtVA 165
          F+CK +F M T+ ++ + + S + ++ + V IW ++
Sbjct:  105 AFICKFIHYFFTVMsLVsIFTLAAMSVDryVAIVHSRRSSSLRVSRNALLGVGF-IWALS 163

Query:  166 SLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFMSMFGKLYPL--LAFG--LPLFFASF 220
          + P + + H + + C P + K Y + FG LPL F
Sbjct:  164 IAMASPvAYHQRLfHRDSNQTFCWEQWPN-----KLHKKAYVVCTfVfGYLLPLLLICF 217

Query:  221 YFWRAYDQCKKRGTKTQNLRNQIRSKQVTMLLSIAIISAVLWLPEWVAWLWVWHLKAAG 280
          + + + K+ K + +++ K+ +L + ++ + WLP V LW A
Sbjct:  218 CYAKVLNHLHKK-LKNMSKKSEASKKKTAQTVLVVVVVFgisWLPPhHVHLWAEF--GAF 274

Query:  281 PAPPQGFI--ALSQVLMFSISSANPLIFLVMSEEFREGLKGVWKWMITKKPPTVSESQE 337
          P P F + L +S SS NP+I+ +SE FR+ K V+K + + P SE++E
Sbjct:  275 PLTPASFFFRITAHCLAYSNSSVNPIIYAFLSENFRKAYKQVfKCHVCDESPr-SETKE 332

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Figure 4

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>sp:NY2R_BOVIN-NEUROPEPTIDE Y RECEPTOR TYPE 2 (NPY2-R).
      Length = 384

Score = 153 bits (383), Expect = 5e-37
Identities = 93/308 (30%), Positives = 164/308 (53%), Gaps = 7/308 (2%)

Query: 47 DEDEDVTNSRTFFAAKIVIGMALVGIMLVCGIGNFIFIAALVRYKKLRNLTNLLIANLAI 106
          D + ++ +S      ++V+ +A  I+L+ IGN + I  +++K +R +TN  IANLA+
Sbjct: 38 DSEPELIDSTKLIEVQVVLILAYCSIILLGVIGNSLVIHVVIKFKSMRTVTNFFIANLAV 97

Query: 107 SDFLVAIVCCPFEMDYYVVRQLSWEHGHVLCSTVNYLRTVSLYVSTNALLAIAIDRYLAI 166
          +D LV+ +C PF + Y ++ +  W+ G VLC  V Y + +++ VST  L  IA+DR+  I
Sbjct: 98 ADLLVNTLCLPFTLTITLMGE--WKMGPVLCPLVPYAQGLAVQVSTITLTVIALDRHRCI 155

Query: 167 VHPLRPRMKCQTATGLIALVWTVSILIAIPSAYFTTETVLVIVKSQEKIFCGQIWPVDQQ 226
          V+ L  ++  Q +  +I L W VS L+A P A F  +++ I+  E + C + WP +++
Sbjct: 156 VYHLESKISKQISFLIIGLAWGVSALLASPLAIFREYSLIEIIPDFEIVACTEKWPGECK 215

Query: 227 -LYYKSYFLFIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLRCRRKTVLV 285
          +Y  Y L  I +V P+ ++  Y RI  +L  PG  +  +R  R+KT  +
Sbjct: 216 GIYGTIYSLSSLLILYVLPLGIISFSYTRIWSKLNHVSPGAHDHYHQR---RQKTTKM 272

Query: 286 LMCILTAYVLCWAPFYGFTIVRDFPTVFVKEKHYLTAFYIVECIAMNSMINTLCFVTV 345
          L+C++  ++ W P + F + D  V + K Y  F +  IAM ++ N L +  +
Sbjct: 273 LVCVVVVFVSWLPLHAFQLAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 331

Query: 346 KNDTVKYF 353
          ++  K F
Sbjct: 332 NSNYRKAF 339

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Figure 5

>sp|P97926|OXYR_MOUSE OXYTOCIN RECEPTOR (OT-R).

Length = 388

Score = 164 (57.7 bits), Expect = 8.9e-22, Sum P(2) = 8.9e-22

Identities = 57/166 (34%), Positives = 84/166 (50%)

Query: 24 WGLNLTGQGAP-----ASGPPSR-----RVRLVFLGVILVVAVAGNTTVLCRLCGGG 71
W + L LG G P +GPP R RV + L +IL +A++GN VL L
Sbjct: 9 WSIELDLGSGVPPGAEGNLTAGPPRRNEALARVEVAVLCLILFLALSGNACVLLAL---- 64

Query: 72 GPWAGPKRRKMDFLLVQLALADLYACGGTALSQLAWELLGEPRAATGDLACRFLQLLQAS 131
K ++ F + L++ADL L QL W++ R DL CR ++ LQ
Sbjct: 65 -RTTRHKHSRLFFFMKHLADIADLVVAVFQVLPQLLDITF--RFYGPDLLCRLVKYLQVV 121

Query: 132 GRGASAHVLVLIALLERRRAVRLPHGRPLPARA--LAALG-WLLALLLALPPAFV 182
G AS +L++L++L+R A+ P R L R LA L WL L+ ++P +
Sbjct: 122 GMFASTYLLLLMSLDRCLAICQPL-RSLRRRTDRLAVLATWLGCLVASVPQVHI 174

Score = 155 (54.6 bits), Expect = 8.9e-22, Sum P(2) = 8.9e-22

Identities = 49/161 (30%), Positives = 85/161 (52%)

Query: 217 CHGIFAPLPRWHLQVYAFYEAVAGFVAPVTVLGVACGHLLS--VWW--RHRPQAPAAAAP 272
C +F + W + Y + +A ++ PV VL AC L+S +W R + A AAAA
Sbjct: 187 CWAVF--IQPWGPKAYVTWITLAVYIVPVIVLA-ACYGLISFKIWQNLRLKTAATAAAAAAE 243

Query: 273 WSASPG-----RAPAPSALPRAKVQSLKMSLLLALLFVGCELPYFAARLAAAWS-SG 323
S + G R + + +AK++++KM+ ++ L F+ C P+F ++ + W +
Sbjct: 244 GSDAAGGAGRAALARVSSVKLISKAKIRTVKMTFIIIVLAFIVCWTPFFVFQMWVWDVNA 303

Query: 324 PAGDWEGEGLSAAALRVVAMANSALNPFVYLFFQAGDCRLRRQLRKRLGSLCCA 376
P E A+ ++A NS NP++Y+ F L +L +R LCC+
Sbjct: 304 PK---EASAFIIAM-LLASLNSCCNPWIYMLFTG---HLFHELVQRF--LCCS 347

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Figure 6

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>sp|Q91178|GPRX_ORYLA PROBABLE G PROTEIN-COUPLED RECEPTOR (FRAGMENT).
      Length = 428

Score = 823 (289.7 bits), Expect = 9.8e-83, P = 9.8e-83
Identities = 182/422 (43%), Positives = 266/422 (63%)

Query:   2 ESSPIPQSSGNSSTLGRVPQTPGPSTASGVPEVGL----RDVASESVALFFMLLLDLTAV 57
          ++SP+ S + S      P P+      P+VG+      +      +      LF M+ L+L A+
Sbjct:   5 KTSPMITSDHISNFSTGLFGPHPTVP---PDVGVVTSSQSQMKDLFGLFCMVTNLIAL 61

Query:  58 AGNAAVMAVIAKTPALRKVFVHLCCLVDLLAALTLMPLAMLSSSALFDHALFGEVACRL 117
          N VM IA+ P L+KF FV HLC VD+L A+ LMPL ++SSS F +F + C++
Sbjct:  62 LANTGVMVAIARAPHLKKFAFVCHLCAVDVLCAILMPLGISSSPFFGTVVFTILECQV 121

Query:  118 YLFLSVCFVSLAILSVSAINVERYYYVHPMRYEVRMTLGLVASVLVGWVKALAMASVP 177
          Y+FL+V + L+IL+++AI+VERY+Y+VHPMRYEV+MT+ LV V++ +W K+L +A V
Sbjct:  122 YIFLNVFLIWLSILTITAISVERYFYIVHPMRYEVKMTINLVIGVMLLIWFKSLLLALVT 181

Query:  178 VLGRVSWEEGAPSVPPGCSLQWSHSAQCFLVVVFAVLVYLLPLLLILVVYCSMFRVARV 237
          + G + +      CSL SHS +F V+F V+ FL P+++I VY ++++VAR
Sbjct:  182 LFGWPPYGHQSSIAASHCSLHASHSRLRGVFAVLCVICFLAPVVVIFSVYSVAVYKVAR 241

Query:  238 AAMQHGP-LPTWME-TP-RQRSESLSSRSTMVTSSGAPQT-TPHRTFGGGKAAVLLAVG 293
          AA+Q P +PTW + +P + RS+S++S++T++T+ PQ +P R F GGKAA+ L +
Sbjct:  242 AALQQVPAVPTWADASPAKDRSDSINSQTTIITRTLPQRLSPERAFSGGKAALTAFIV 301

Query:  294 GQFLLCWLPYFSFHLYVALSAQPISTGQVESVVTWIGYFCFTSNPFFYGCLNRQIRGELS 353
          GQFL+CWLP+F FHL ++L+ S G +E V W+ Y F NP FYG LNRQIR EL
Sbjct:  302 GQFLVCWLPFFIFHLQMSLTGSMKSPGDLEEAVNWLAYSSFAVNPSFYGLLNRQIRDELV 361

Query:  354 K-QFVCFFKPAPEEELRLPSREGSIEENFLQFLQGTGCPSESWSRPLPSPKQ-EPPAVD 411
          K + C +P E+ S EGS +ENFLQF+Q T SE+ S +P+ E A
Sbjct:  362 KFRRCVTPV---EIGPSSLEGSFQENFLQFIQRTSSSSETHPSFANSNPRNMENQA-- 416

Query:  412 FRIPGQIAEE 421
          +IPGQI EE
Sbjct:  417 HKIPGQIPEE 426

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Figure 7

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>sp|P23749|RTA_RAT PROBABLE G PROTEIN-COUPLED RECEPTOR RTA.
      Length = 343

Score = 461 (162.3 bits), Expect = 2.3e-44, P = 2.3e-44
Identities = 121/323 (37%), Positives = 178/323 (55%)

Query:      2 NQTLNSSGTVESALNYSRGS-TVHT-AYL----VLSSLAMFTCLCGMAGNSMVIWLLGFR 55
              NQ      G E+  YSRG T+  A L    V + + + CLCG+ GN +V+W  GF
Sbjct:     13 NQNKMCPGMSEALELYSRGFLTIEQIATLPPPAVTNYIFLLLCLCGLVGNGLVLWFFGFS 72

Query:     56 MHRNPFCIYILNLAADLLFLFSMASTLSLETQPLVNT-TDKVHELMKRLMYFAYTVGLS 114
              + R PF IY L+LA+AD ++LFS A    L    + + D V + + +   + G+S
Sbjct:     73 IKRTPFSIYFLHLASADGIYLFSAVIALNMGTFLGSPDYVRRVSRIVGLCTFFAGVS 132

Query:    115 LLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCCKFL--KFNE 172
              LL AIS +RC+SV+FP+W+  RP+ LSA VC LLW L  L+  + + FC  FL  + +
Sbjct:    133 LLPAISIERCVSVIFPMWYWRRRPKRLSAGVCALLWLLSFLVTSIHNYFCM-FLGHEASG 191

Query:    173 DRCFRVDMVQAALIMGVLT PVM T LSSLTLFVWVRRSSQWRRQPTRLFVVVLASVLVFLI 232
              C +D+    L+  + P+M L  L L + V   +++ R++ +L  VVLA V VFL+
Sbjct:    192 TACLNMDISLGILLFFLCPLMVLPCALILHVECRARR-RQRSAKLNHVLAIVSVFLV 250

Query:    233 CSLPLSIYWFVLYWL-SLPPEMQVLCFSLSR LSSSVSSSANPVIYFLVGSRRSHRLPTRS 291
              S+ L I WF L+W+ +P          ++ L  ++SSA P++YFL G  +S RL
Sbjct:    251 SSIYLGIDWF-LFWVFQIPAPFPEY---VTDLCICINSSAKPIVYFLAGROKSQRL-WEP 305

Query:    292 LGTVLQQALRE--EPELEGGETPTVGTNEM 319
              L V Q+ALR+ EP      TP  T EM
Sbjct:    306 LRVVFQRALRDGAEPGDAASSTPNTVTMEM 335

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Figure 8

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>sp|Q98907|P2Y3_CHICK P2Y PURINOCEPTOR 3 (P2Y3) (NUCLEOSIDE DIPHOSPHATE
RECEPTOR).
Length = 328

Score = 452 (159.1 bits), Expect = 2.0e-43, P = 2.0e-43
Identities = 85/185 (45%), Positives = 116/185 (62%)

Query:   15 CQFSEKYKQVYLSLAYSIIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL 74
          C F E++KQV L L YS++F+LGLPLN V+ W K + T Y++NL +ADLLYV
Sbjct:   13 CTFHEEFKQVLLPLVYSVVFLGLPLNAVVGQIWLARKALTRTTIYMLNLAMADLLYVC 72

Query:   75 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCSVHQFLGVCHPLCSLPY 133
          LP LI Y+ D WPGF+ CK V F FY NL+GSIL LTCISV +++G+CHPL S
Sbjct:   73 SLPLLIYNYTQKDYWPGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHK 132

Query:   134 RT-RRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 192
          + ++ WL + W +V+ Q LPT F+ T + + YD++ + F YGI LT
Sbjct:   133 KKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPDRSTSYFPYGITLT 192

Query:   193 LSGFL 197
          ++GFL
Sbjct:   193 ITGFL 197
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Figure 9

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>sp|002824|A1AA_RABIT ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A-ADRENOCEPTOR)
      (ALPHA-1C ADRENERGIC RECEPTOR).
      Length = 466

Score = 295 (103.8 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31
Identities = 66/215 (30%), Positives = 113/215 (52%)

Query:   8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLQVTN 67
          S  S+SS+  P  +  P++++  I+  +L  +  +GNI++ L  +  L  VT+
Sbjct:   5 SGNASDSSNCTHPPA--PVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLSVTH 62

Query:  68 RFIFNLLVTDLLQISLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 127
          +I NL V DLL S V P+  + +W  FC  ++ L  AS+ ++ V+S+
Sbjct:  63 YYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVISI 122

Query:  128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
          DRY+ + +PL YP+ +TQRRG  L  W  +++ S  PL+GW Q A D+  +C  +
Sbjct:  123 DRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDDET-ICQI--N 179

Query:  188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ 222
          P Y + S +  +PL +++A Y  V+  A+R+
Sbjct:  180 EEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKRE 214

Score = 106 (37.3 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31
Identities = 23/75 (30%), Positives = 41/75 (54%)

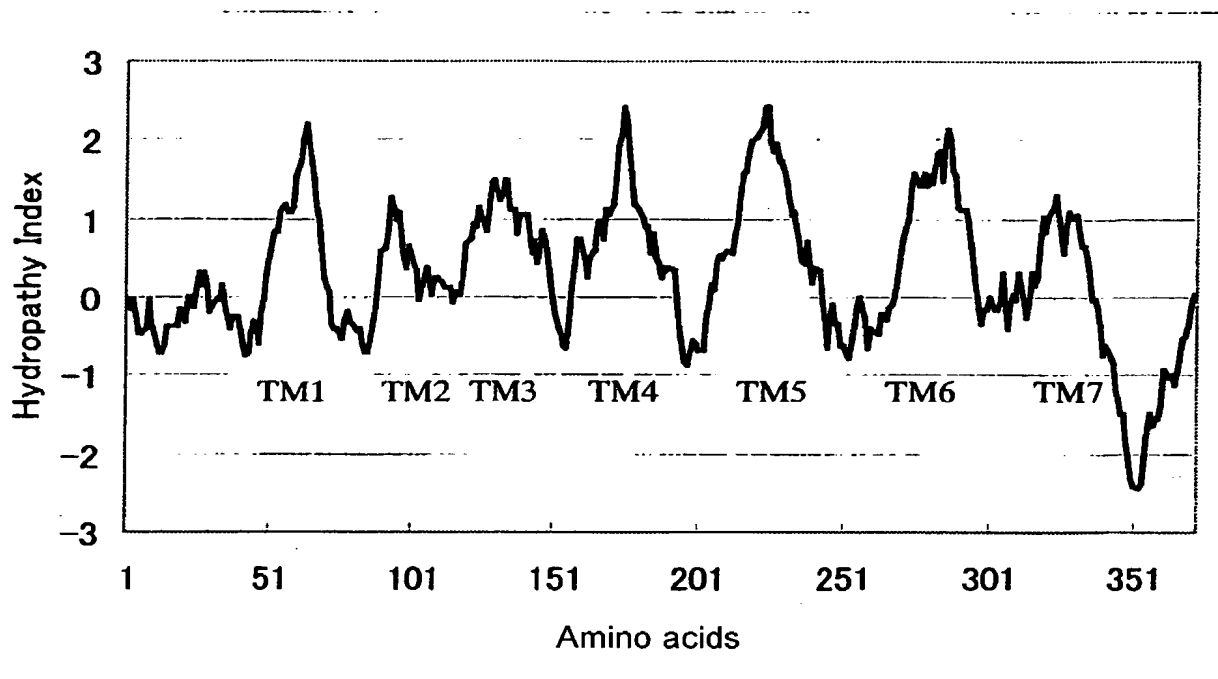
Query:  396 KAAKVIFIIIFSIVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFQCCIHPPYVG 455
          KAAK + I++ +VL  P+  +  +  +  + P+ V  I+ WL +L  CI+P +Y
Sbjct:  269 KAAKTLGIVVGCFLVLCWLPFFLVMPIGSFFP-DFKPPETVFKIVFWLGYLNSCINPIIYP 327

Query:  456 YMHKTIKKEIQDMLK 470
          +  KK  Q++LK
Sbjct:  328 CSSQEFKKAFQNVLK 342

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Figure 10



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Figure 11

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X64878      MEGALAN---WSA-EAA-NASAAPPGAEG-----NRTAGPPRRNEALARVEVAVLCLIL
U82440      MEGELAN---WST-EAV-NSSAAPPGAEG-----NCTAGPPRRNEALARVEVAVLCLIL
X93313      MEGLCLNL---DCS-ELP-NSSWVNSSMENQNHSSNSTROPLKRNEEVAKVEVTVLALIL
X87783      MEEMFKEQDF-WSFNESRSTVGNETFGG-----NQTVNPLKRNEEVAKVEVTVLALVL
AF184966    -----MEKPGNITLHP-----NGSDPFGRNREEVAQIEIMVLSITF
X76321      -----MGRIANQTAS-----NDTDPFGRNREEVAKMEITVLSVTF
AF147743    MKNFSFPMQD-STHQTESPPHRLLSLTNKS-----DPVGRPERDEQLAQVEIAVLGVIF
GPRv8      MPANFTEGSFDSSGTQTLDS SPVACTETVTFTEVVEGKEWGSFYYSFKTEQLITLWVLF
AE003754    -----MKCDHTLFFALFQTEQFAVLWILF
                                     ..*:::

TM1 ***** TM2 *****
X64878      LLALSGNACVLLALRTTRQKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGPDL
U82440      FLALSGNACVLLALRTTRHKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGPDL
X93313      FLALAGNICVLLGIYINRHKHSRMYFFMKHLSIADLVVAIFQVLPQLIWDITFRFYAPDL
X87783      FLALAGNLCVLIAYTAKHTQSRMYLMKHLSIADLVVAVFQVLPQLIWDITFRFYGPDL
AF184966    VVAVIGNVSULLAMYNTHKKMSRMHLFIKHLADLVVAFFQVLPQLCWEITYRFFGPDF
X76321      FVAVIGNLSVLLAMHNTKKKSRMHLFIKHLADLVVAFFQVLPQLCWEITYRFFGPDF
AF147743    LTASVGNFILIILVLRWRKKLSRMYVFMHLHSIADLVVAFFQVLPQLIWDITDVFIGPDF
GPRv8      VFTIVGNSVVLFTSWR-RKKKSRMTFFVTQLAITDSFTGLVNIITDINWRFTGDFAPDL
AE003754    TVIVLGNSAVLFVFMFINKNRKS RMNYFIKQALADLCVGLLNVLTDIWRITISWRAGNL
          **:::  ::**::: *::: *::: *:::

@***** TM3 ***** TM4 *
X64878      LCRLVKYLQVVG MFASTYLLLLMSLDRCIAICQPLRS LRRRT--DRLAVLATWLGCLVAS
U82440      LCRLVKYLQVVG MFASTYLLLLMSLDRCIAICQPLRS LRRRT--DRLAVLATWLGCLVAS
X93313      VCRVLYLQVVG MFASTYLLLLMSLDRCIAICQPLRS LHRRS--DCVYVLTWILSFLLS
X87783      LCRLVKYLQVTGMFASTYMLVLMSIDRCIAICQPLRS LHKRK--DRCYVIVSWALS LVS
AF184966    LCRIVKHLQVTGMFASTYMMVMMLTDRIYIAICHPLKTLQPTQRSYIMIVSTWMC SLVS
X76321      LCRIVKHLQVLGMFASTYMMVMMLTDRIYIAICHPLKTLQPTQRAYIMIGSTWLC SLLS
AF147743    LCRIKYLLQLLGMFASTYMIIVMTVDRIYQAVCYPMVTFQKKRALWNIPICTSWSISLIS
GPRv8      VCRVRYLQVLLYASTYVLVSLSIDRYHAIYVPMKFLQGEKQ-ARVLIVIAWSLSFLS
AE003754    ACKAIRFSQVCVTYSSTYVLVAMSIDRYDAITHPMNFSKSWKR-ARHLVAGAWLISALFS
          *: : . * : : : : : : : : : : : : : : : : : : : : : :

***** @ ***** TM5 *****
X64878      APQVHIFSLREVADG--VFDCWAVFIQP--WGPKAYITWITLAVYIVPVIVLATCYGLIS
U82440      APQVHIFSLREVADG--VFDCWAVFIQP--WGPKAYITWITLAVYIVPVIVLAACYGLIS
X93313      TPQTVIFSLTEVGNG--VYDCRADFIQP--WGPKAYITWITLAVYIIPVMILSVCYGLIS
X87783      VPQVYIFSLREIGNG--VYDCWGFVQF--WGAKAYITWISLTIIYIIPVAILGGCYGLIS
AF184966    TPQYFIFSLSEVKNGSTVKDCWAHFI EP--WGARAYITWITGGIFLVPVIVLMCYGFIC
X76321      TPQYFIFSLSEIQNGSYVYDCWGHFI EP--WGI RAYITWITVGIFLIPVILMICYGFIC
AF147743    LPQVFI FSKIEISPG--IFECWAEFIQP--WGPRAYVTWILVVIFFIPSTILITCQVKIC
GPRv8      IPTLIIFGKRTLNG--EVQCWALWPDDSYWTP--YMTIVAFVYFIPLTIISIMYGIVI
AE003754    LPILVLYEEKLIQGH--PQCWIELGSPIANQV--YMSLVSATLFAIPALISACYAIV
          *:::  :  : *  :  : *  : : : : : : : : : :

```

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Figure 12

X64878	FKIWQNLRKTAATAAAAEAEPEGAAAGDGGRVALARVSSVKLISKAKIRTVKMTFIIVLAF	***** TM6
U82440	FKIWQNLRKTAATAAAAEAEPEGAAAGDGGRVALARVSSVKLISKAKIRTVKMTFIIVLAF	
X93313	YKIWQNIRLKTVCESNLRST-----SRRATLSRVSSVRLISKAKIRTVKMTFIIVLAY	
X87783	FKIWQNFKRKTKKQDCITLTAA-----SKANALARVSSVKLVSKAKITTVKMTFIIVLAY	
AF184966	HTIWKNIKYKKRKTIPGAAS-----KNGLIGKNSVSSVTISRAKLRTVKMTFIIVLAY	
X76321	HSIWKNIKCK-----TMRGTRNT-----KDMIGKYSVSSVTISRAKLRTVKMTLIIVLAY	
AF147743	KIIRNIIYVKKQNEYQVTNQ-----KQVLPSSRASSVNCISKAMIKTVKMTIIVTVAY	
GPRv8	RTIWIKSKTYETVISNCSOG-----KLCSSYNRGLISKAKIKAIKYSIIIIILAF	
AE003754	KTIWAKCSIFVPTERAGFGA-----APARRASSRGIIPRAKVTVKMTLTIVFVF	
	* : . : * : : * : : . :	
	***** TM7 *****	
X64878	IVCWTPFFFVQMWNSVWDANAPK-----EASAFIIVMLLASLNSCCNPWIYMLFTGHLFHEL	
U82440	IVCWTPFFFVQMWNSVWDANAPK-----EASAFIIVMLLASLNSCCNPWIYMLFTGHLFHEL	
X93313	IVCWTPFFFVQMWNSVWDPNPPK-----EASLFIIVMLLASLNSCCNPWIYMLFTGHLFHDLL	
X87783	IVCWTPFFFVQMWNSVWDPEAPR-----EAMPFIISMLLASLNSCCNPWIYMFAGHLFHDLL	
AF184966	IICWAPFFTQMWNSVWDENFQYADSENTAVTISALLASLNSCCNPWIYMFSGHLLQDFM	
X76321	IVCWAPFFIVQMWNSVWDENFSDDSSENAAVTISALLASLNSCCNPWIYMLFSGHLLYDFL	
AF147743	VLCWSPFFIAQLNSVWFPSGIT-----EGSAFTIIMLLGNLNSCTNPWIYMYFCGHIPIY	
GPRv8	IICWSPYFLFDILDNFNLLPDT-QERFYASVIQNLPALNSAINPLIYCVFSSSISFP--	
AE003754	IICWSPYIIFDLLQVFGQIPHS-QTNIAIATFIQSLAPLNSAANPLIYCLFSSQVFRTLS	
	: **: *: : : : : : * ** . ** * : :	
X64878	QR-----FLCCSASYLKGRRLG-ETSASKSN-----SSSFVLSHRSSSQRSQS	
U82440	QR-----FLCCSASYLKGRRLG-ETSTSKSN-----SSSFVLSHRSSSQRSQS	
X93313	QS-----FLCCSARYLKTQQQS-DLSASRKN-----SSTFVLSRKSQSISITQS	
X87783	QS-----LLCCSTLYLKSSQCRCDQEHDSRKN-----CSTYVIKSTSS-QRSITQSS	
AF184966	NC-----FAMCRRANADFKED-SDSSIRRT-----LLTKMTN-RSPTGSTGNWRD	
X76321	RC-----FPCCKKPRNMLQED-SDSSIRRT-----LLTKLAAGRMTNDGFGSWRD	
AF147743	-----CTNKQLENTSAQ-EDSVVTGS-----IHLVD-RDPEENSTCA-	
GPRv8	-----CREQRSQDSRMT-FRERTER-----HEMQILS-KP-EF-----	
AE003754	RFPPFKWFTCCCKSYRNNSQNRCHTVGRRLHNSCDMSMTLTSLTVSRRSTNKTNARVV	
	* :	
X64878	TA-----	
U82440	TA-----	
X93313	TA-----	
X87783	IT-----	
AF184966	LDNSPK--TSIQME-----	
X76321	PCNSRKSSQSIGLDCFCCKSSQCLEHDCSRKSSQCIPLDCSRKSSQCIPLDCSRKSSQCMS	
AF147743	-----	
GPRv8	-----	
AE003754	ICERPTKVVTVPAMSERRGVSLKGNTDIL-----	
X64878	---	
U82440	---	
X93313	---	
X87783	---	
AF184966	---	
X76321	KES	
AF147743	---	
GPRv8	---	
AE003754	---	

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Figure 13

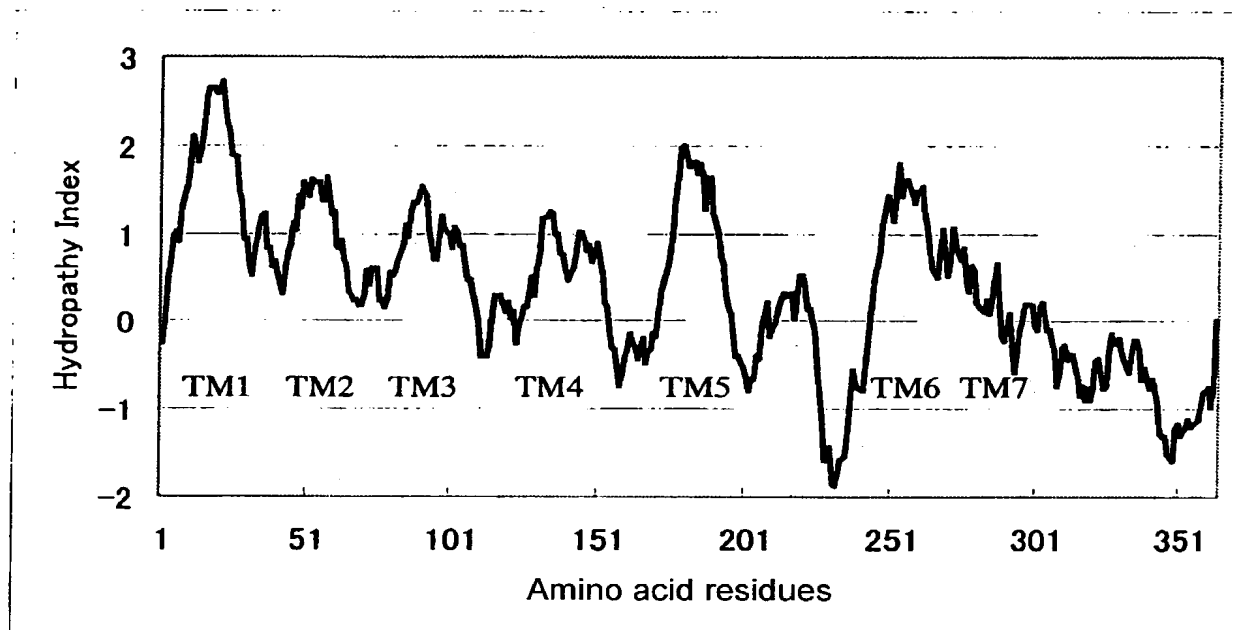
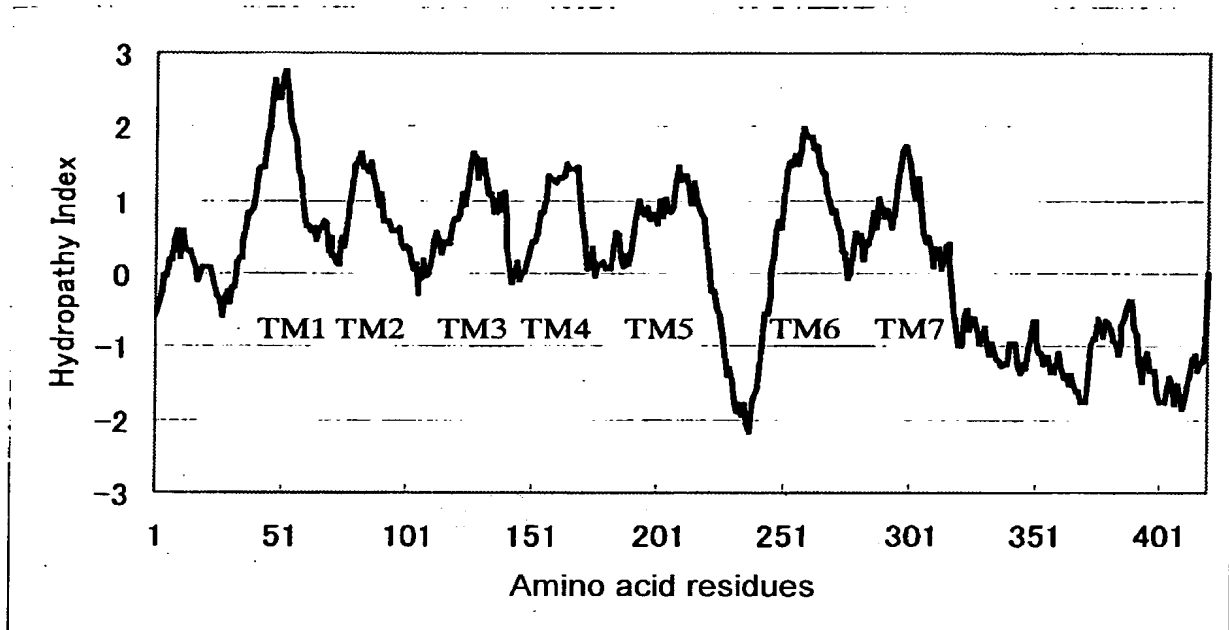


Figure 14

GPRv12_ORF AF208288	<p>##### TM1 #####</p> <p>MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLSLGHLLLAALDM</p> <p>MNSWDAGLAGLLVGTIGVSLLSNGLVLLCLLHSADIRRQAPALFTLNLTcGNLLCTVVM</p> <p>*. * ##### . : * : *</p>
GPRv12_ORF AF208288	<p>##### @##### TM3 #####</p> <p>PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLP</p> <p>PLTLAGVVAQRQPAGDRLCRLAFLDTFLAANSMLSMaALSIDRWVAVVFPLSYRAKMRL</p> <p>* : * * * : * * : * : * : * * * * * : * : * * * * * * * * * * * *</p>
GPRv12_ORF AF208288	<p>##### TM4 ##### @ #####</p> <p>RYAGLLLGCawGQSLAFSGAALGCSWLGYSsAFASCSLRLPPEPERPRFAAFTATLHAVG</p> <p>RDAAFMVAYTWLHALTFPATALALSNLGFHQLYASCTLCsRRPDERLRFavFTSAFHALS</p> <p>* * : : : * : * : * : * : * * * * * : * * * * * * * * * * * *</p>
GPRv12_ORF AF208288	<p>TM5 #####</p> <p>FVLPLAVLCLTSLQVHRVARRHCQRMDTVTMKALALLADLHPSVRQRCLIQKRRRRHRAT</p> <p>FLLSFIVLCFTYLVKLVKVARFHCKRIDVITMQTLVLLVDIHPSVRERCLEEQRRRQRAT</p> <p>* : * : *</p>
GPRv12_ORF AF208288	<p>##### TM6 #####</p> <p>RKIGIAIATFLICFAPYVMTRLaELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP</p> <p>KKISTFIGTFLVCfAPYVITRLVELFSTAPIDSHWGVLSKCLAYSKAASDPFVYSLLRHQ</p> <p>: * * . * : * * : *</p>
GPRv12_ORF AF208288	<p>FRQVLagMvHRLlKRTPrPaSTHdSSLDVagMvHQLlKRTPrPaSTHngSVDTENDSCLQ</p> <p>YRRsCKELLNRIFNRR---SIHSVGLTGDSHSQNI LPVSE-----</p> <p>: * : : * : *</p>
GPRv12_ORF AF208288	<p>QTH</p> <p>---</p>

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Figure 15



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Figure 16

```

*****
***** TM1 *****
1 MLAAAFADSN SSSMNVSFAH LHFAGGYLPS DSQDWRTIIP ALLVAVCLVG FVGNLCVIGI 60

*****
## ***** TM2 *****
61 LLHNAWKGP SMIHSLILNL SLADLSLLLF SAPIRATAYS KSVWDLGWV CKSSDWFIHT 120

*****
@***** TM3 ***** ***** TM4 *****
121 CMAAKSLTIV VVAKVCFMYA SDPAKQVSIH NYTIWSVLVA IWTVASLLPL PEWFFSTIRH 180

*****
@ ***** TM5 *****
181 HEGVEMCLVD VPAVAEEFMS MFGKLYPLLA FGLPLFFASF YFWRAYDQCK KRGTKTQNL 240

*****
***** TM6 ***** ***** TM7 **
241 NQIRSKQTV MLLSIAIISA VLWLPEWVAW LWVWHLKAAG PAPPQGFIAL SQVLMFSS 300

*****
*****
301 ANPLIFLVMS EEFREGLKGV WKWMITKKPP TVSESQETPA GNSEGLPDKV PSPEPASIP 360
361 EKEKPSSPSS GKGKTEKAEI PILPDVEQFW HERDTVPSVQ DNDPIWEHE DQETGEGVK 419

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Figure 17

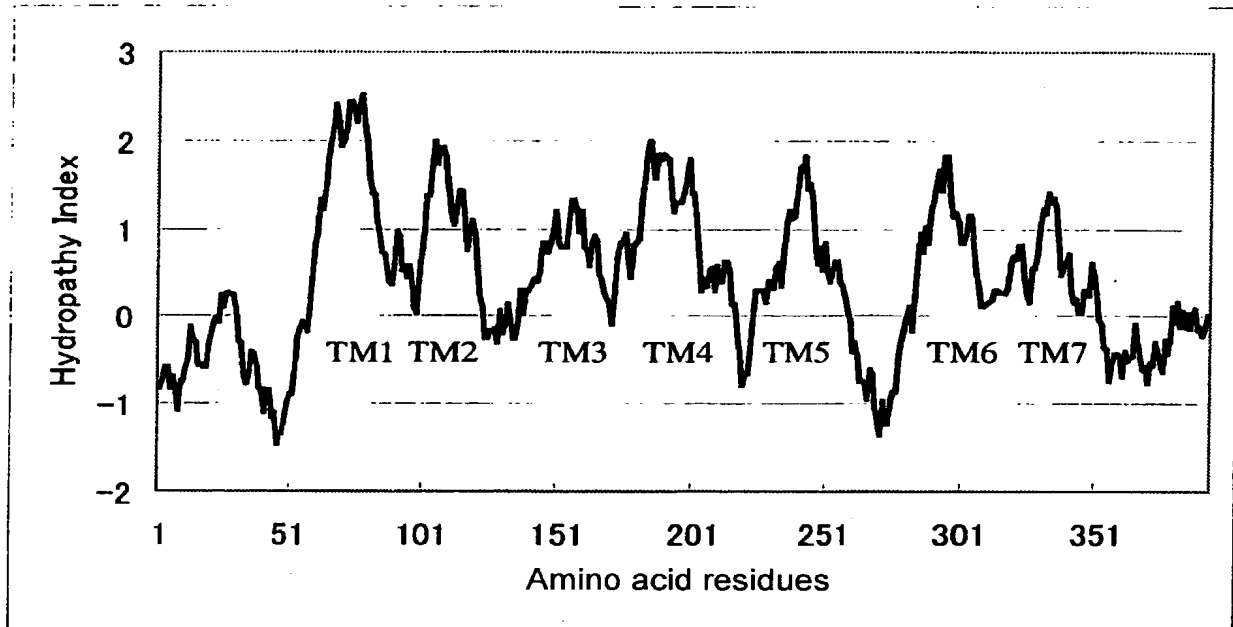


Figure 18

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GPRv21      -----METTMGFMDNATNTSTSFLSVLNPHGAHA-TSFPFN
AL121755    -----
AF236082    -----METT VGALGENTTDTFTDFFSALDGHEAQT-GSLPFT
U42766      -----MGPI GAEADENQTV EENKVEQYGP-----
U76254      -----MGPI GAEADENQTV EENKVEQYGP-----
U42389      -----MGPI GAEADENQTV EENKVEQYGP-----
U50144      -----MKMGPLGAEADENQTV EENKV DQFGPG-----
D86238      -----MVLKMGPVGAEDEN-QTVEVKVEPYGPG-----
M81490      MYYIAHQQPMLRNEDDN YQEGYFIRPD PASLIYNTTALPADDEGSNYGYGSTT-TLSGLQ
AF037444    --MSMANSENSTSLFGIKRHADV TGPHSASHDV IPSNTSVYYDHASNYESVLSTTSTM

                                     ##### TM1
GPRv21      FSYSDYDMPL----DEDEDVTNSR-----TFFAAKIVIGMALVGIMLVCGIGNFIF
AL121755    --YG DYDLPM----DEDEDMTKTR-----TFFAAKIVIGIALAGIMLVCGIGNFVF
AF236082    FSYGDYDMPL----DEEEDVTNSR-----TFFAAKIVIGMALVGIMLVCGIGNFIF
U42766      QTTPRGELVP----DPEPELIDST-----KLIEVQVV LILAYCSI ILLGVIGNSLV
U76254      QTTPRGELVP----DPEPELIDST-----KLIEVQVV LILAYCSI ILLGVIGNSLV
U42389      QTTPRGELVP----DPEPELIDST-----KLIEVQVV LILAYCSI ILLGVIGNSLV
U50144      HTTPRGELAP----DSEPELIDST-----KLIEVQVV LILAYCSI ILLGVIGNSLV
D86238      HTTPRGELPP----DPEPELIDST-----KLIEVQV ILIAYCSI ILLGVGNLSLV
M81490      FETYNITVM MNFSCDDYDLL SEDMW-----SSAYFKI IVMYLYIP IFALIGNGT V
AF037444    LKLTDLVTPFNASEPD PESNGSDTG GHAAISEQPMYAKVI ILMYVLI I LVAVGGNLLF

          * : .                :: :   *: .   ** .
#####           ##### TM2 #####           @#####
GPRv21      IAALVRYKKLRNLTNLLIANLAISDFLVAI VCCPFEMDYVVRQLSWEHGHVLC TSVNYL
AL121755    IAALTRYKKLRNLTNLLIANLAISDFLVAI ICCPFEMDYVVRQLSWEHGHVLCASVNYL
AF236082    ITALARYKKLRNLTNLLIANLAISDFLVAI VCCPFEMDYVVRQLSWEHGHVLCASVNYL
U42766      IHVVIKF KSMRTVTNFFIANLAVADLLVNTLC LPFTLT YTYTLMG--EWKMG PVLCHLPYA
U76254      IHVVIKF KSMRTVTNFFIANLAVADLLVNTLC LPFTLT YTYTLMG--EWKMG PVLCHLPYA
U42389      IHVVIKF KSMRTVTNFFIANLAVADLLVNTLC LPFTLT YTYTLMG--EWKMG PVLCHLPYA
U50144      IHVVIKF KSMRTVTNFFIANLAVADLLVNTLC LPFTLT YTYTLMG--EWKMG PVLCHLPYA
D86238      IHVVIKF KSMRTVTNFFIANLAVADLLVNTLC LPFTLT YTYTLMG--EWKMG PVLCHLPYA
M81490      CYIVYSTPR MRTVTNYFIAS LAIGDI LMSFFCEPSSFISLFILN-YWPFGLALCHFVNYS
AF037444    SYVIVMPYKMR SVTNLFL LNLAISDIVKAVICNPFAFIANLILL-YWPYGEFM CQVV TYI

          :   :*.** :. :*.**.:   .* * :   :   * * :* * *
## TM3 #####           ##### TM4 #####
GPRv21      RTVS LYVSTNALLAI AIDRYLAIVHPLRPRMKCQTATGLIALVWT VSILIAIPSAYFTTE
AL121755    RTVS LYVSTNALLAI AIDRYLAIVHPLKPRMN YQTASFLIALVWMVSILIAIPSAYFATE
AF236082    RTVS LYVSTNALLAI AIDRYLAIVHPLRPRMKCQTAAGLIFLWSVSILIAIPAAYFTTE
U42766      QGLAVQVSTI TLTVIALDRHRCIVYHLESKISKRSFLI IGLAWGISALLASPLAIFREY
U76254      QGLAVQVSTI TLTVIALDRHRCIVYHLESKISKRSFLI IGLAWGISALLASPLAIFREY
U42389      QGLAVQVSTI TLTVIALDRHRCIVYHLESKISKRSFLI IGLGWRI SALLASPLAIFREY
U50144      QGLAVQVSTI TLTVIALDRHRCIVYHLESKISKQSFLI IGLAWGVSALLASPLAIFREY
D86238      QGLAVQVSTI TLTVIALDRHRCIVYHLESKISKRSFLI IGLAWGISALLASPLAIFREY
M81490      QAVSVLV SAYTLVAISI DRYIAIMWPLKPRITKRYATFI IAGVWFIALATALPIPIVSGL
AF037444    QVVAVFLSAFTLVAMSVD RYVAI LKPMRPRLSKRAFITMATIWILSLSAPLPTAITSRV

          :   :*: :* :.:**.*: .*:   :   :   * : :   . * .

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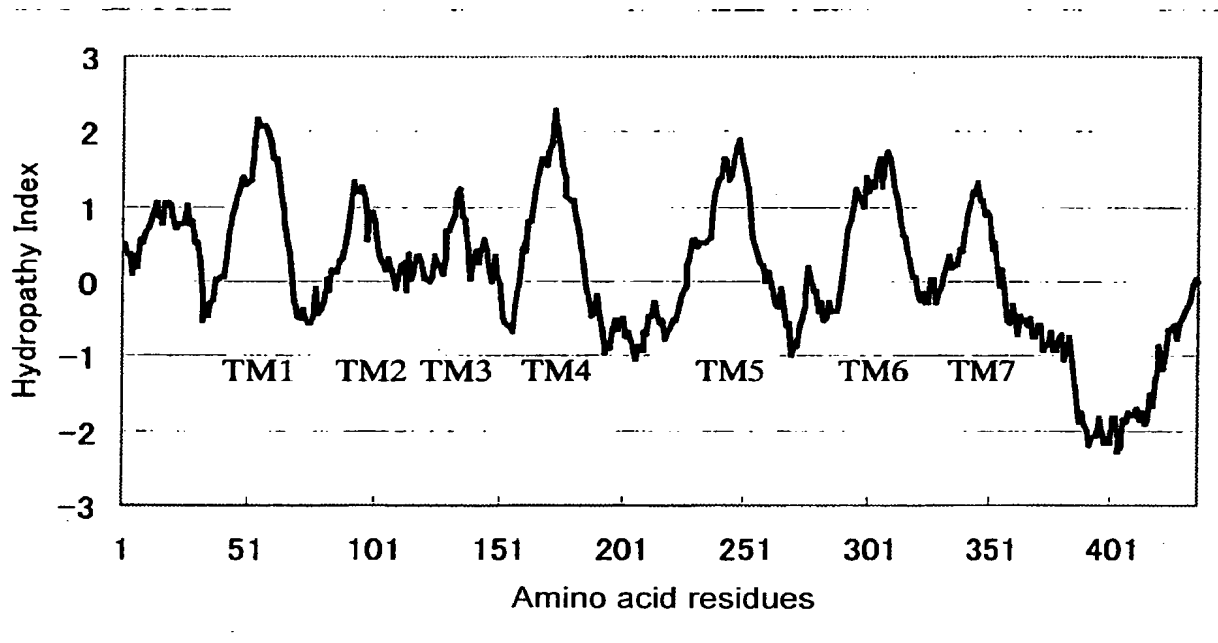
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Figure 19

		0	***** TM5 *****
GPRv21	TVLVIVKSQ--EKIFCGQIWPVDQQ--LYYKSYFLFIFGIEFVGPVVTMTLCYARISRELW		
AL121755	TVLVIVKSQ--EKIFCGQIWPVDQQ--LYYKSYFLFIFGVEFVGPVVTMTLCYARISRELW		
AF236082	TVLVIVERQ--EKIFCGQIWPVDQQ--FYRSYFLLVFGLEFVGPVVTMTLCYARVSRELW		
U42766	SLIEIIPDF--EIVACTEKWPGEKSIYGTVYSLSSLLILYVPLPLGIISFSYTRIWSKLG		
U76254	SLIEIIPDF--EIVACTEKWPGEKSIYGTVYSLSSLLILYVPLPLGIISFSYTRIWSKLG		
U42389	SLIEIIPDF--EIVPCTEKWPAAEKSIYGTVYSLSSLLILYVPLPLGIISFSYTRIWSKLG		
U50144	SLIEIIPDF--EIVACTEKWPGEKGIYGTIYSLSSLLILYVPLPLGIISFSYTRIWSKLG		
D86238	SLIEIIPDF--EIVACTEKWPGEKSVYGTVYSLSTLLILYVPLPLGIISFSYTRIWSKLG		
M81490	DIPMSPWHTKCEKYICREMWPSRSQ---EYYTTLSEFALQFVPLPLGLIFTYARITIRVW		
AF037444	TKQSNSTGL-----CLEHFENDHN---RYIYSIVIMMLQYFVPLAVITVTNTHIGYIVW		
		* : : : *	: : : : *
		***** TM6 *****	
GPRv21	FKAVPG-FQTEQIRKRLRCRRKTVLVLMCILTAYVLCWAPFYGFTIVRDFPPTVFVKEKH		
AL121755	FKAVPG-FQTEQIRKRLRCRRKTVLVLMCILTAYVLCWAPFYGFTIVRDFPPTVFVKEKH		
AF236082	FKAVPG-FQTEQIRRTVRCRRRTVLGLVCVLSAYVLCWAPFYGFTIVRDFPPTVFVKEKH		
U42766	NHVSPG-AANDHYHQR---RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE		
U76254	SHVSPG-AANDHYHQR---RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE		
U42389	NHVSPG-AANDHYHQR---RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE		
U50144	NHVSPG-AANDHYHQR---RQKTTKMLVCVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE		
D86238	NHVSPG-AASDHYHQR---RHKMTKMLVCVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE		
M81490	AKRPPGEAETNRDQRMARSKRMVKMMLTVVIVFTCCWLPFNILQLLLN--DEEFAHNDP		
AF037444	IKKTPGEAEEDRRMAASKRRLVKMIIVVVIYAVCWLPVHVITLVGD-HNPDIYNQPH		
		: **	: : : : : : : : : : *
		***** TM7 *****	
GPRv21	YLTAFYIVECIAMNSMINTLCFVTVKNDTVKYFKKIML-----LHWKASYNGGKS		
AL121755	YLTAFYVVECIAMNSMINTVCFVTVKNNMKYFKKMML-----LHWKPSQRGSKS		
AF236082	YLTAFYVVECIAMNSMINTLCFVTVRNNTSKYLKRIIR-----LQWRASPSGSKA		
U42766	YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDAIHSEV		
U76254	YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDAIHSEV		
U42389	YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDAIHSEV		
U50144	YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDAIHSEV		
D86238	YKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLSAFR-----CEQRDAIHSEV		
M81490	LPYVWFAFWLASHCCYNPIICYMNAFRSGFVQLMHRMPGLRRWCCLRSVGDRMNAT		
AF037444	MNVVNLCAQWLASHSCYNPFVYFSLSATFRRNLRRMTHACRLKQKR-LRQHLSMRSSRA		
		: **	: : : : : : : : : *
GPRv21	S-----ADLDLKTIGM---PATEEVDCIRLK-----		
AL121755	S-----ADLDLRTNGV---PTTEEVDCIRLK-----		
AF236082	S-----ADLDLRTTGI---PATEEVDCIRLK-----		
U42766	SVTFKAK-----KNLEVRKNSG---PNDSFTEATNV-----		
U76254	SVTFKAK-----KNLEVRKNSG---PNDSFTEATNV-----		
U42389	SVTFKAK-----KNLEVRKNSG---PNDSFTEATNV-----		
U50144	SVTFKAK-----KHLQVTKNNG---PNDSFTETTIV-----		
D86238	SMTFKAK-----KNLEVKKNNG---PTDSFSEATNV-----		
M81490	SGTGPALPLN--RMNTSTTYISARRKPRATSLRANPLSCGETSPLR-----		
AF037444	DAWDRDTEVYGSAESIPSKVSAGSLHSSNRGAHVNTSSGEWQCLKEKKLKGVSNDMYL		

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Figure 20



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Figure 21

```

**
##### TM1 **
1 MEDLFSPSIL PPAPNISVPI LLGWGLNLT L GQGAPASGPP SRRVRLVFLG VILVVAVAGN 60

*****
#### ##### TM2 #####
61 TTVLCRLCGG GGPWAGPKRR KMDFLLVQLA LADLYACGGT ALSQLAWELL GEPRAATGDL 120

*****
@ ##### TM3 ##### ##### TM4 #####
121 ACRFLQLLQA SGRGASAHV VLIALERRA VRLPHGRPLP ARALAALGWL LALLLALPPA 180

*

#####
### @ ##### TM5
181 FVVRGDSPSP LPPPPPTSL QPGAPPAARA WPGQRRCHGI FAPLPRWHLQ VYAFYEAVAG 240

*****
#####
241 FVAPVTVLGV ACGHLLSVWW RHRPQAPAAA APWSASPGRA PAPSALPRAK VQSLKMSLLL 300

*****
# TM6 ##### ##### TM7 #####
301 ALLFVGCELP YFAARLAAW SSGPAGDWEG EGLSAALRVV AMANSALNPF VYLFFQAGDC 360

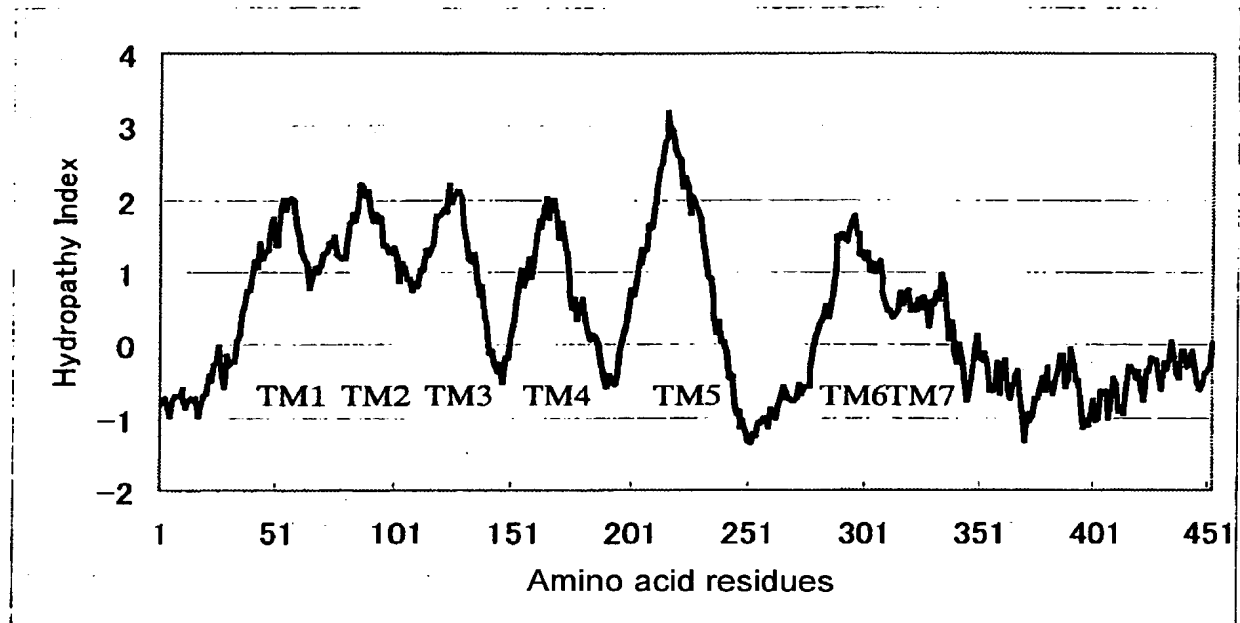
361 RLRRQLRKRL GSLCCAPQGG AEDEEGPRGH QALYRQRWPH PHYHHARREP LDEGGLRPPP 420

421 PRPRPLPCSC ESAF

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Figure 22



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Figure 23

HSH2R_1	-----	-----	-----	-----
D49783	-----	-----	-----	-----
M32701	-----	-----	-----	-----
U25440	-----	-----	-----	-----
S57565	-----	-----	-----	-----
S73473	-----	-----	-----	-----
M74716	-----	-----	-----	-----
U64032	MTFRDLLSVTFEGPRPDI	SAGGSGAGGGAGAGAGODT	ASSESPAVGGVPGAAGGGGGG	
L41147	-----	-----	-----	-----
GPRv47	-----	-----	-----	-----
D43633	-----	-----	-----	-----
HSH2R_1	-----	-----	-----	###
D49783	-----	NG-----	TASSFCLOSTACKIT-----	ITV
M32701	-----	MAP-----	NG-----	TASSFCLOSTACKIT-----
U25440	-----	MIS-----	NG-----	TGSSFCLOSPPCRIT-----
S57565	-----	MAF-----	NG-----	TVPSFCMDFTVYKVT-----
S73473	-----	MEP-----	NG-----	TVHSCCLDSMALKVT-----
M74716	-----	MAPWPHKNGS-----	LAFWSDAPTLDPSAANTSGLPG-VPW-AAAL	
U64032	VVGAGSGEDNRSSAGEPGGAGGGGE-----	VNGTAAVGGLVVSASVSG-----	VGW	
L41147	-----	MVP-----	EPGPT-----	ANSTPAWGAGPPSAPGGSG-----
GPRv47	-----	MESSPI PQSSGNSSTLGRVPQTPGPSTASGVPEVGLRDV-ASESVALF		
D43633	-----	MMADKTSPIITSDHSISNFSTGLFGPHPTVPPDVGVVTSSQSQMKOLFGLF		
HSH2R_1	### TM1 #####	##### TM2 #####		
D49783	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
M32701	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
U25440	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
S57565	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
S73473	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
M74716	VLAVLILITVAGNVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSCK			
U64032	AGALLALATVGGNLLVITAIARTPRLQITNVFVTSLATADLVVGLLVMPPGATLALTGH			
L41147	AGALLALATVGGNLLVITAIARTPRLQITNVFVTSLATADLVVGLLVMPPGATLALTGH			
GPRv47	FLAAFILTAVAGNLLVILSVACNRHLQVTNYFIVNLAVADLLSATVLPFSATMEVLGF			
D43633	ALCVVIALTAANSLIALICTQPALRNTSNFFLVSLFTSOLMVGLVMPPLNALYGR			
	FMLLLDLTAVAGNAAMVAVIAKTPALRKFFVVFHCLVDLLAALTLMPLMLSSSALFDH			
	CMVTLNLIALLANTGVMAIARAPHLKKFAFVCHLCVAVDVLCAILLMPLGISSSPFFGT			
	. : . * : : : * . : : :			
HSH2R_1	### @##### TM3 #####	##### TM4		
D49783	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
M32701	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
U25440	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
S57565	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
S73473	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
M74716	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLIW			
U64032	WPLGATGCELWTSVDVLCVTASIETLCALAVDRYLAVTNPLRYGTLVTKRRARAAYVLVW			
L41147	WPLGATGCELWTSVDVLCVTASIETLCALAVDRYLAVTNPLRYGTLVTKRRARAAYVLVW			
GPRv47	WAFGRAFCDVAAAVDVLCCCTASISLCTISVDRYVGVVHSLKYPAMTERKAAAIALLLW			
D43633	WVLARGLCLLWTAFDVMCCSASILNLCISLDYLLILSPLRYKLRMTPLRALALVLGAW			
	ALFGEVACRLYLFLSVCFVSLAII SVSAIINVERYYYVHPMRYEVRMTLGLVASVLVGVW			
	VVFTILECQVYIFLNVFLIWLISLITITAIISVERYFYIVHPMRYEVKMTINLVIGVMLLIIN			
	: * : : . * : * : : : * : : * : * : : *			

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Figure 24

HSR2R_1	*****	@	***** TM5 *****
D49783	VISITLSFLSIHLGWN---SRNETSKGNHTTSKCN-----VQVNEVYGLVDGLVTFYLPLLIMCI		
M32701	VISITLSFLSIHLGWN---SRNETSKGNHTTSKCK-----VQVNEVYGLVDGLVTFYLPLLIMCI		
U25440	VISITLSFLSIHLGWN---SRNETSSFNHTIPKCK-----VQVNLVYGLVDGLVTFYLPLLVMCI		
S57565	VISITLSFLSIHLGWN---SRNETSKDNDTIVKCK-----VQVNEVYGLVDGLVTFYLPLLIMCI		
S73473	IVSATVSFAPIMSQWVRVGADAEAEQCHSNPRCCS-----FASNMPYALLSSVSFYLPLLVMLF		
M74716	IVSATVSFAPIMSQWVRVGADAEAEQCHSNPRCCS-----FASNMPYALLSSVSFYLPLLVMLF		
U64032	AVLVVS-MGPLLGWK-----EPVPPD-ERFC-----GITEEVGYAVFSSLSFYLPMAVIVV		
L41147	SLAALASFLPLLGLWH-----ELGHARPPVPGQC-----RLLASLPFVLVASGLTFFLPSPAICF		
GPRv47	VKALAMASVPVLGRVS-NEEGAPSVPPG-----CSLQWSHSAYCQLFVVVFAVLYFLLPLLILV		
D43633	FKSLLA-LVTLFGWPPYGHQSSIAASH-----CSLHASHSRLRGVFAVLFVCIFLAPVVVIFS		
	:	*	: : * *
HSR2R_1	*		
D49783	TYRIFRVARDAQAKRID-HIS-----SWKAATIR-----		
M32701	TYRIFKVARDAQAKRIN-HIS-----SWKAATIR-----		
U25440	TYRIFKVARDAQAKRIH-HMG-----SWKAATIG-----		
S57565	TYRIFKVARDAQARRIN-HIG-----SWKAATIR-----		
S73473	TYRIFKVARDAQAKRIN-HIS-----SWKAATIR-----		
M74716	VYARVFVAKRQRRLRLRELGRFPPEESPRSPSRSPSPATVGTPTAS-----DGVPSGCR		
U64032	VYARVFVAKRQRRLRFVRELGRFPPEESPRSPSRSPSPATVGTPTAS-----DGVPSGCR		
L41147	MYCRVYVARSTTRSLEAGVKRERKASEVVLRIHCRGAASGADGAPGTRGAKGHTFRSS		
GPRv47	TYCRILLAARKQAVQVASLTG-----MASQASETLQVPRTP--R--PGVESADS		
D43633	VYCSMFRVARVAAMQHGPLPTWETP-----RQRSESLSSR--S--TMTVSSGA		
	VYSAVYKVARSAALQQVPAVPTWADAS-----PAKORSDSINSQTT-----IITRTLP		
	* : * :		
HSR2R_1	***** TM6 *****		*****
D49783	-----EHRATVTLAAVMGAFIICWFYPTAFVYRGLRGDDAINEWLEAIVLWLG		
M32701	-----EHKATVTLAAVMGAFIICWFYPTAFVYRGLRGDDAINEVLEAIVLWLG		
U25440	-----EHKATVTLAAVMGAFIICWFYPTAFVYRGLRGDDAINEAFEAVLWLG		
S57565	-----EHKATVTLAAVMGAFIICWFYPTAFVYRGLRGDDAINEAVEGIVLWLG		
S73473	RPARLLPLG-EHRALRTLGLIMGIFSLCWLFFFLANVLRALVGPSLVPSGVFIALNWLG		
M74716	RPARLLPLG-EHRALRTLGLIMGIFSLCWLFFFLANVLRALVGPSLVPSGVFIALNWLG		
U64032	LSVRLKFSREKKAAKTLAIVVGCVFVLCWFFFFVLPGLSLFPQLKPSGVFVFIWLG		
L41147	RRLATKHSRKALKASLTGLIGLGMFFVTWLPFFVANIQAVC--DCISPLFDVLTWLG		
GPRv47	PQTTPHRTFGGKAADVLLAVGGQFLCWLPHYFSFHLVVALSAQPISTGQVESVVTWIG		
D43633	QRLSPERAFSGKAALTAFIVGQFLVCWLPHYFHLQMSLTGSMKSPGDLEEAVNWLAY		
	: * * : * * : * * :		: * * :
HSR2R_1	TM7 *****		
D49783	ANSALNPILYAALNRDFTGYQQLFCCRLANRNSHKTSLRSNASQLSRTQSREPR---Q		
M32701	ANSALNPILYAALNRDFTGYQQLFCCRLANRNSHKTSLRSNASQLSRTQSREPR---Q		
U25440	ANSALNPILYATLNRDFTAYQQLFRCRPAASHNAQETSLRSNSSLARNQSREPR---R		
S57565	ANSALNPILYAALNRDFTAYQQLFHCCKFASHNSHKTSLRLNNSQLNRSQCQEP---W		
S73473	ANSALNPILYAALNRDFTAYQQLFHCCKFASHNSHKTSLRLNNSQLNRSQCQEP---W		
M74716	ANSALNPILYCR-SPDFRDAFRLL-CSYGGRGPEEP--RVVTFPASPVASR-----		
U64032	ANSALNPILYCR-SPDFRDAFRLL-CSYGGRGPEEP--RVVTFPASPVASR-----		
L41147	FNSCVNPLIYPCSSREFKRAFLRLRCQCRRRRRRRPLRVYGHWRASAGGGPHPCAL		
GPRv47	CNSTMNPILYPLFMRDFKRALGRFLPCPRCPRERQAS-LASPSLRTHSGPRPGLS---L		
D43633	FCFTSNPFYGLNRQIRGELSKQFVCFKPAPEEELRLPSREGSIEENFLQ-----F		
	SSFAVNPSFYGLLRNQIRDELVKFRCCVTQPVETGP--SSLEGSFQENFLQ-----F		
	** * : : *		

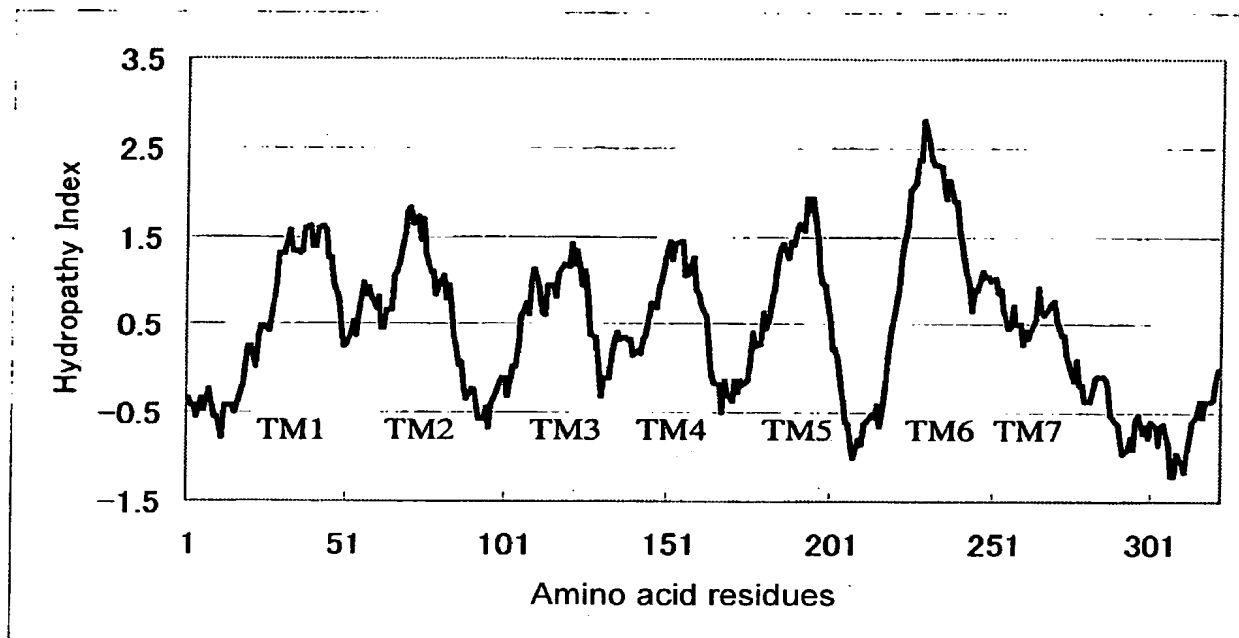
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Figure 25

HSH2R_1	QEEKPLKLQVWSGTEVT-----
D49783	QEEKPLKLQVWSGTEVTAPQGATDR-----
M32701	QEEKPLKLQVWSGTEVTAPRGATDR-----
U25440	QEDKPLNLQVWSGTEVTAPQGATNR-----
S57565	QEEKPLKLQVWSGTELTHPQGNPIR-----
S73473	QNS-PLNR--FDGYEGERP-FPT-----
M74716	QNS-PLNR--FDGYEGERP-FPT-----
U64032	SAGAALPGAALALTAAPAPSSAAAPGQAAGAGRRKPPCAFREWRLLGPLRRPTTQLRAK
L41147	QQVLPLPLPPDSDSDSAGSGSSGLRLTAQLLLPGEATQDPPLPTRAAAANFFNIDPA
GPRv47	LQGTGCPSESWSRPLSPKQEPVDFRIPGQIAETSEFLEQQLTSDIIMSDSYLRPA
D43633	IQRTSSSSETHPSFANSNP-RNMENQAHKIPGQIPPEQA-----
HSH2R_1	-----
D49783	-----
M32701	-----
U25440	-----
S57565	-----
S73473	-----
M74716	-----
U64032	VSSLSHKIRAGGAQRAEAACALRSEVEAVALSVARDVAEDNTCQAYELADYRNLRETDI
L41147	EPELRPHPLGIPTN-----
GPRv47	ASPRLES-----
D43633	-----

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Figure 26



GPRv51
 M35297

***** TM1 #
 -----MNQTLNSSGTVESALNYSRGSTVHTAYLVLSLAMFTCLCGMA
 MAGNCSWEAHSTNQNMCPGMSEALELYSRGFLTIEQIATLPPPAVTNYIFLLCLCGLV
 . . . * * : ** . . * . : : : *****.

GPRv51
 M35297

***** TM2 *****
 GNSMWIWLGLFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVN-TTDKVHELMK
 GNGLVLWFFGFSIKRTPFSIYFLHLASADGIYLFKAVIALLNMGTFLGSFPDYVRRVSR
 .:*:*:*:* :*..*:*:*:*:* :*** * * : * * : . :

GPRv51
 M35297

***** TM3 *****
 RLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSS
 IVGLCTFFAGVSLLPAISIERCVSVIFPMWYWRRRPKRLSAGVCALLWLLSFLVTSIHNY
 : : .*:***.** :*:*:*:*:* :*:*:**** **.*** *.:*.:. .

GPRv51
 M35297

***** TM5 *****
 FCSKFLKFNE-DRCFRVDMVQAALIMGVLTVPVNTLSSLTLFVWVRRSSQWRRQPTRLFY
 FCMFLGHEASGTACLNMDISLGILLFFLCPLMVLPCLALILHVECRARRRRQRS-AKLNH
 ** : : . *.:*:* : *.: : : *.*.*.*:*:* * . : : : * . : *

GPRv51
 M35297

***** TM6 *****
 VVLASVLVFLICSLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGS
 VVLAIVSVFLVSSIYLGIDWFLFWVFQIP---APFPEYVTDLCICINSSAKPIVYFLAGR
 **** * ***.:*:* *.* *:*:* : : * : : *.*:*:*:*:* *

GPRv51
 M35297

***** TM7 *****
 RRSRLPTRSLGTVLQQALRE--EPELEGGETPTVGTNEMGA-----
 DKSQRLWEP-LRVVFQRALRDGAEPGDAASSTPNTVTMEMQCPSGNAS
 :*:** * .*:*:***: ** ...*.*. * ** .

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Figure 28

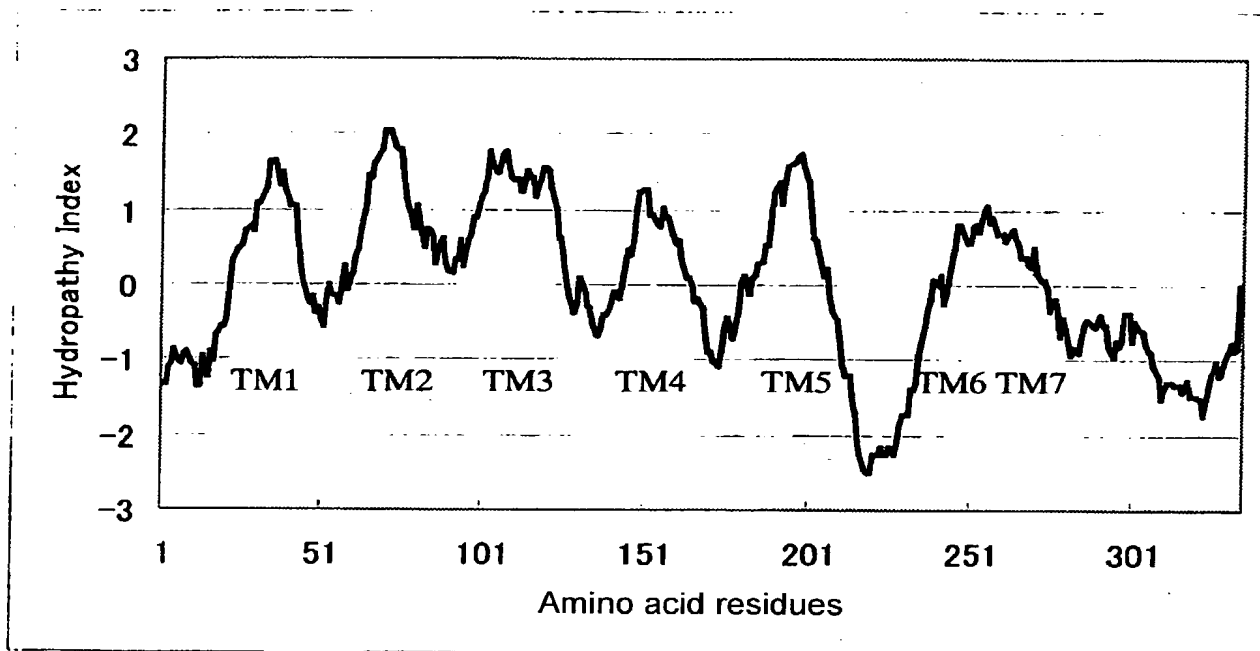


Figure 29

```

Y14705          -----MTSAESLLFTSLGPSPPSGDGDGRFNEEFKILLPMSYAVVFLGLAL
AJ277752        -----MTSADSLFTSLGPSPPSGDGDCKFNEEFKILLPLSYAVVFLGLAL
AF031897        ---MDAPVRMFSLAPWTPTPTPWLGNTTAAAEAKCVFNEEFKILLPISYGIVFVVLGLPL
X99953          MTEDIMATSYPTFLTTPYLPMLKLLMNLNDTEDICVFDEGFKFLLPLVSYSAVFMVGLPL
AF069555        -----MSMANFTA---GR-----NSCTFQEEFKQVLLPLVYSVVFLGLPL
X98283          -----MSMANFTG---GR-----NSCTFHEEFKQVLLPLVYSVVFLGLPL
D63665          -----MERDNGTIQAPGLPP---TTCVYREDFKRLLLPPVYSVVFLVGLPL
GPRv71          -----MEKVDMNTSQ---EQ-----GLCFSEKYKQVYLSLAYSIIFILGLPL
                * : * * : * . * . : : * * .

##### TM1 #####

Y14705          NAPTLWLFLFRLRPWDATATYMFHLALSDTLVYVLSLPTLVYVYAARNHWPFGTGLCKFVR
AJ277752        NAPTLWLFLFRLRPWDATATYMFHLALSDTLVYVLSLPTLVYVYAARNHWPFGTGCKFVR
AF031897        NSWAMWIFVSRMRPNWNTTTFMFLAISDTLYVFSLPTLVYVYADRNNWPFGKVFCIVR
X99953          NIAAMWIFIAKMRPNWNTTTFMFLALSDTLVYVLSLPTLVYVYADKNNWPFGVLCCKLVR
AF069555        NAVVIGQIWLARKALTRTTIYMLNLATADLLYVCSLPLLINYTKQDYWPFGDFTCKFVR
X98283          NAVVIGQIWLARKALTRTTIYMLNLAMADLLYVCSLPLLINYTKQDYWPFGDFTCKFVR
D63665          NVCVIAQICASRRTLRSVYTLNLALADLLYACSLPLLINYARGDHWPFGLACRLVR
GPRv71          NGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL-LPFLIITYSLDRWPFGELLCKLVH
                * : : : : : * : * : * * . * * : * : : * * : * : * :

##### TM2 #####

Y14705          FLFYWNLYCSVLFTCISVHRYLGICHPLRAIRWGRPR-FASLLCLGVWLVVAGCLVPNL
AJ277752        FLFYWNLYCSVLFTCISVHRYMGICHPLRAIRWGRPR-FAGLLCLGVWLVVAGCLVPNL
AF031897        FLFYANLYSSILFTCISVHRYMGICHPIRSLKWKTK-HARLICVGVWLVVTICLIPNL
X99953          FLFYANLYSSILFTCISVHRYMGICHPIRSLKWKTK-HARLICVGVWLVVTICLIPNL
AF069555        FQFYTNLHGSILFTCISVQRYMGICHPLASWHKKKGKKTWLVCAAVWFIVIAQCLPTF
X98283          FQFYTNLHGSILFTCISVQRYMGICHPLASWHKKKGKKTWLVCAAVWFIVIAQCLPTF
D63665          FLFYANLHGSILFTCISFQRYLGICHPLAPWHKRGRRAAWVCGVWLVVTAQCLPTA
GPRv71          FLFYINLYGSILLTICISVHQFLGVCHPLCSLPYRTRR-HAWLGTSTTALVVLQLLPTL
                * * * : * : * : * : : : * : * : : : * : * :

##### TM3 #####

Y14705          FFVTTNANGTTILCHDHTTLPEEFHDYVYFSSAVMVLFLGLPFLITLVCYGLMARRLYRPL
AJ277752        FFVTTNANGTTILCHDHTTLPEEFHDYVYFSSITMVLFGFPFLITLVCYGLMARRLYRPL
AF031897        IFVTTSSKDNSTLCHDHTTKPEEFHDYVHYSSIMALLFGIPFLVIVVCYCLMAKRLCKRS
X99953          IFVTVSPKVKNITCHDHTTRPEDFARYVEYSTAIMCLLFGIPCLIIAGCYGLMTRRLMKPI
AF069555        VFASTGTQRNRTVCYDLSPDRSASYFPYGITLTITGFLLPFAAILACYCSMARILCQKD
X98283          VFASTGTQRNRTVCYDLSPDRSTSYFPYGITLTITGFLLPFAAILACYCSMARILCQKD
D63665          VFAATGIQRNRTVCYDLSPPIILSTRYLPGMALTIVIGFLLPFTALLACYCRMARRLCRQD
GPRv71          AFSHTDYINGQMIWYDMSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFDTGQEPDQARG
                * . . : : * : : . . : : * : : : :

##### TM4 #####

Y14705          PGAGQS---SSRLRSLRTIAVVLTVFAVCFVPFHITRTIYYQAR-LLQADCHVLNIVNVV
AJ277752        PGAGQS---SSRLRSLRTIAVVLTVFAVCFVPFHITRTIYYLAR-LLNAECRVNIVNVV
AF031897        FPSPSPRVPSYKKRSIKMIIVLTVFAICFVPFHITRTLYYTSR-YFQADQCQTLNINFT
X99953          VSGNQQLTPSYKKRSIKTIIFVMIIFAICFMPFHITRTLYYYAR-LLGIKCYALNIVNVT
AF069555        ELIGLAVH-KKKDKAVRMIIVVIVFSISFFPFHLTKTIYLIVRSSPTLPCPTLQAFAlA
X98283          ELIGLAVH-KKKDKAVRMIIVVIVFSISFFPFHLTKTIYLIVRSSASLPCPTLQAFAlA
D63665          GPAGPVAQ-ERRSKAARMVAVVAVFVISFLPFHITKTAYLAVRSTPGVSCPVLFTFAAA
GPRv71          EPHEDRQHSPSQVHPDHTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQ
                : : : . . * : : :

```

Figure 30

	***** TM7 *****	
Y14705	YKVT RPLASANSCLDPVLYLFTGDKYRNQLQQLCRGSK--PKPR-----	TAASSL
AJ277752	YKVT RPLASANSCLDPVLYLFTGDKYRNQLQQLCRGST--PKRR-----	TTASSL
AF031897	YK ITRPLASINSCLDPI LYFMAGDKYRGRLRRGAAQR--P-R-----	PVPTSL
X99953	YKVT RPLASANSCLDP ILYFLANDRYRRRL I RTVRRRSSVPNRRCMHTNHPQTEPHMTAG	
AF069555	YKCTRPFASMN SVLDPI LFYFTQRKFRESTRYLLDKMS-----	SKWRHD
X98283	YKCTRPFASMN SVLDPI LFYFTQRKFRESTRYLLDKMS-----	SKWRQD
D63665	YKGT RPFASANSVLDPI LFYFTQQKFRRQPHDLLQKLT-----	AKWQRQ
GPRv71	DMEASGECEQLPQPSPVLSFKGGKNRVRL LQKL RQNKLG-----	EHPAGRK
	: : * : *	
Y14705	ALVTLHEES I SRWADTHQDSTFSAYEGDRL-----	
AJ277752	ALVTLHEES I SRWADIHQDSIFPAYEGDRL-----	
AF031897	LALVSPSVDS SVVGSCCNSE-----SRGMGT VWSRGGQ-----	
X99953	PLPVI SAEI I PSNGSMVRDENGEGSREHRVEWTDKE I NQMMNRRST I KRNSTDKNDMKE	
AF069555	HC I TYGS-----	
X98283	HC I SYGS-----	
D63665	RV-----	
GPRv71	RCPGLNRSG-----	
Y14705	-----	
AJ277752	-----	
AF031897	-----	
X99953	NRHGENYLPYVEVVEKEDYETKRENRTTEQSSKTNAEQDELQTQIDSRLKRGKWQLSSK	
AF069555	-----	
X98283	-----	
D63665	-----	
GPRv71	-----	
Y14705	-----	
AJ277752	-----	
AF031897	-----	
X99953	KGAAQENEKGHMEPSFEGETSTWNLLTPKMYGKKORLAKNVEEVGYGKEKELQNFPA	
AF069555	-----	
X98283	-----	
D63665	-----	
GPRv71	-----	

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Figure 31

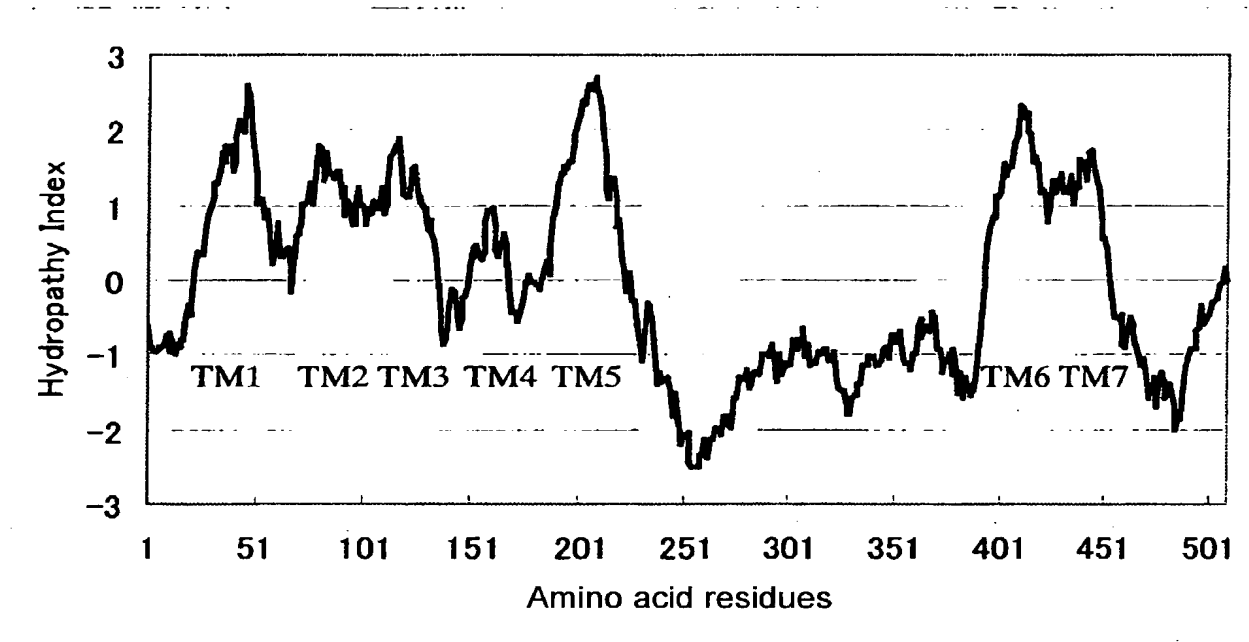


Figure 32

```
U03866 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
L31774 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
D25235 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
D32202 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
D32201 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
AF013261 -----MVFLSGNAS--DSSNCTQPPAP-----VNISKAILLGVILGGLIFGV LGNILV
U81982 -----MVFLSGNAS--DSSNCTHPPAP-----VNISKAILLGVILGGLIFGV LGNILV
U07126 -----MVLLENAS--EGSNCTHPPAP-----VNISKAILLGVILGGLIFGV LGNILV
S71323 MVPVLDNMTPSSVTI--NCSCNSHVLAPE----LNTVKAVVLGMVLGIFI LFGVIGNILV
D63859 -----MT PSSVTI--NCSCNSHVLAPE----LNTVKAVVLGMVLGIFI LFGVIGNILV
AF091890 -----MSLNSSLSCRKELSNLTEEEGG-----EGGVIIITQFIAIVITI FVCLGNLYI
GPRv72 -----MTSTCTNST--RESNSSHTCMPLSKMPI SLAHGIIRSTVLVI FLAASFVGNI V
          :      * .           :       :     :   :    **:::

***                ##### TM2 #####              @#####
U03866 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
L31774 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
D25235 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
D32202 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
D32201 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
AF013261 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFEVLGYWAFGRVF CNIWAADV
U81982 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFE ILGYWAFGRVF CNIWAADV
U07126 ILSVACHRHLSVTHYY IVNLAVADLLLTSTVLPFS AIFE ILGYWAFGRVF CNIWAADV
S71323 ILSVVCHRHLQT VTYYF IVNLAVADLLLSSTV LPFSAIFEILD RVFGRVC NIWAADV
D63859 ILSVVCHRHLQT VTYYF IVNLAVADLLLSSTV LPFSAIFEILD RVFGRVC NIWAADV
AF091890 VVT LYKKSYLLT SNKFVS LT SNFLLSVLV LFVVT SSIRREW IFGVWC NF SALLYL
GPRv72 ALVLQRKPQL QVTNRFI FNLLVTDL LQIS LVAPWV VATSV PLFWPL NSHF CTAL VS L TH
        : : : * :: ...* :*: * *: . .. * :: .* . :

# TM3 #####                 ##### TM4 #####
U03866 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
L31774 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
D25235 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
D32202 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
D32201 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
AF013261 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRRGL MALLCV WALSLVIS IG P L FGWR-
U81982 LCCTASI I SLCVIS IDRYIGV SYPLRYPTIV TQRR GLR ALL CV W AFSL VIS VG P L FGWR-
U07126 LCCTASIMGLCI ISIDRYIGV SYPLRYPTIV TQRR GVR ALL CV WV LS VIS IG P L FGWR-
S71323 LCCTASIMS LCVIS DRYIGV SYPL RYPA IMTK RRALL AVML LWVLS VI SI GP L FGWK-
D63859 LCCTASIMS LCVIS DRYIGV SYPL RYPA IMTK RRALL AVML LWVLS VI SI GP L FGWK-
AF091890 LISSASM TLGV IAID RYYY AVL YPMVP MK IT GNRA VMAL VYIW LHSL IG CL PP L FGWS
GPRv72 LFAFAS VNTIV VVSVD RYLSI IHPLSYPS KMT QR RG YLLL YGTWI VA I L Q STPPLY GWGQ
* . **: : :.:** . : :* * * *. : * :.. **.**:
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Figure 33

```
##      0      ***** TM5 *****
U03866  QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
L31774  QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
D25235  QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
D32202  QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
D32201  QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
AF013261 QPAPEDETICQINE--EPGYVLFSA LGSFY LPLA I I LVMYCRVYV VAKRESRGLK----S
U81982  QPAPDDEETICQINE--EPGYVLFSA LGSFY VPLT I I LAMYCRVYV VAKRESRGLK----S
U07126  QPAPEDETICQINE--EPGYVLFSA LGSFY VPLA I I LVMYCRVYV VAKRESRGLK----S
S71323  EPAPEDETVCKITE--EPGYA I FSA VGSFY LPLA I I LAMYCRVYV VAKRESRGLK----E
D63859  EPAPEDETVCKITE--EPGYA I FSA VGSFY LPLA I I LAMYCRVYV VAKRESRGLK----E
AF091890 VEFDEFKWM CVA AWHREP GYTA FWQ I WCA LF PFL VML VCYGF I FRVARV KARKVH----C
GPRv72  AAFDERNALCSMIWGASPSYTI LSVVSF I VIPL I VMI ACYSVVFCAARRQHALLYNVKRH
      : : : *      . * . : :      . * : : : * : : . * : : :

*****
U03866  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
L31774  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
D25235  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
D32202  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
D32201  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
AF013261 GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
U81982  GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKA AKT LGI VVG-
U07126  GLKTDKSDSEQVTLRIHRKNVPAEGGVSSAKNKTHFSVRLLKFSREKKA AKT LGI VVG-
S71323  GQKIEKSDSEQVILRMHRGNTTVSED--EALRSRTHFALRLLKFSREKKA AKT LGI VVG-
D63859  GQKIEKSDSEQVILRMHRGNTTVSED--EALRSRTHFALRLLKFSREKKA AKT LGI VVG-
AF091890 GTVVIVEEDAQRTG--RKNSTSTST--SSGSRRAFQGVVYSANQCK--ALITILVVLG-
GPRv72  SLEVRVKDCVENEDEEGA EKKEEFQD--ESEFRQHEGEVKAKEGRMEAKDGLKAKEGS
      . : : : : : : : : : : : : : : *

***** TM6 *****
U03866  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
L31774  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
D25235  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
D32202  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
D32201  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
AF013261 ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
U81982  ----CFVLCWLP----FFLVMP IGSFFPD----FKPPETVFK I VFNLGYLNSCIN----
U07126  ----CFVLCWLP----FFLVMP IGSFFPD----FKPSETVFK I VFNLGYLNSCIN----
S71323  ----CFVLCWLP----FFLVLP IGSIFPA---YRPSDTVFK I TFWLGYFNNSCIN----
D63859  ----CFVLCWLP----FFLVLP IGSIFPA---YRPSDTVFK I TFWLGYFNNSCIN----
AF091890 ----AFMVTWGP----YMVV IASEALWGK---SSVSPSLETWATWLSFASAVCH----
GPRv72  TGTSESSVEARGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGE
      . : .      * . : :      . . .
```

Figure 34

U03866	*****
L31774	-PIIYPCSSQEFK---KAFQNVLR IQCLCRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D25235	-PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D32202	-PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
D32201	-PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHPPSQAVEGQHK-
AF013261	-PIIYPCSSQEFK---KAFQNVLR IQCLCRKQSSKH---ALGYT-LHPPSQAVEGQHK-
U81982	-PIIYPCSSQEFK---KAFQNVLR IQCLRRKQSSKH---ALGYT-LHAPSQALEGQHK-
U07126	-PIIYPCSSQEFK---KAFQNVLR IQCLRRRQSSKH---ALGYT-LHPPSQALEGQHR-
S71323	-PIIYLCSNQEFK---KAFQSL LGVHCLRMT PRAHHHLSVGQSQTQGHSLT I SLD SKG
D63859	-PIIYLCSNQEFK---KAFQSL LGVHCLRMT PRAHHHLSVGQSQTQGHSLT I SLD SKG
AF091890	-PLIYGLWN-----KTVRKEL LGMCF GDRYYREP-----FVQR--QRTSRLFS ISNR-
GPRv72	DDMEFGEDD INFSEDDVEAVN I PESLPPSRNSNSNP---PLPRCYQCKAAKVIF I I FS
U03866	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARVRSKS
L31774	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARVRSKS
D25235	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARVRSKS
D32202	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARTKSRS
D32201	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARGHTPM
AF013261	DMVRIPVGSRETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--SCTTARRGMD C
U81982	DMVRIPVGSGETFYRISKTDG--VCEWKFFSSMPRGSARITVSKDQS--ACTTARVRSKS
U07126	DMVRIPVGSGETFYRISKTDG--VCEWKFFSSMPQGSARITVSKDQS--ACTTARVRSKS
S71323	APCRLSPSSSVALSRTPSSRD--SREWRVFSGGP INSG--PGPTEAG--RAKVAKLCNKS
D63859	APCRLSPSSSVALSRTPSSRD--SREWRVFSGGP INSG--PGPTEAG--RAKVAKLCNKS
AF091890	-ITDLGLSPHLTALMAG-----GQPLGHS--SSTGDTG--FSCSQDSGN--
GPRv72	VVLSLGPYCF L AVLAVWVDVETQVPQWVIT I I I WLFLLQCCIHPYVYGYMHKTIKKEIQD
U03866	FLQVCCCVGPS-TPSLDKN--HQVPTIKVHT I SLENGEEV-----
L31774	FLQVCCCVGPS-TPSLDKN--HQVPTIKVHT I SLENGEEV-----
D25235	FLEVCCCVGPS-TPSLDKN--HQVPTIKVHT I SLENGEEV-----
D32202	VTRLECSG---MILAHCN--LRLPGSRDSPASASQAAGTTGDVPPGRRHQAQLIFVFLV
D32201	T-----
AF013261	RYFTKNCR---EHIKHVN--FMPPWRKGLEC-----
U81982	FLQVCCCVGPS-TPNPGEN--HQVPTIKIHT I SLENGEEV-----
U07126	FLQVCCCVGSS-APRPEEN--HQVPTIKIHT I SLENGEEV-----
S71323	LHRTCCCILRARTPTQDPAPLGDLP TIKI HQLSLSEKGESV-----
D63859	LHRTCCCILRARTPTQDPAPLGDLP TIKI HQLSLSEKGESV-----
AF091890	-LRAL-----
GPRv72	MLKKFFCKEK--PPKEDSH--PDLPGTEGGTEGKIVPSYDSATFP-----
U03866	-----
L31774	-----
D25235	-----
D32202	ETGFHHVGQDDL D L L T S
D32201	-----
AF013261	-----
U81982	-----
U07126	-----
S71323	-----
D63859	-----
AF091890	-----
GPRv72	-----